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Gly	<sub>ອ</sub>	
Glu	GAA	
Cys	T G	170
Ser	TTCC	
Leu	C T	
Asn	AAC	0
Thr	A C C	160
Arg	<b>V</b> 0 0	
Asn	AAT	

### FIGURE 2 (cont.)

Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu CTC C C A G G A A A A A A C T G G T C T G C T T T A C T G 230 240

Thr Ala Val Val Ile Ile Leu Thr Ile Ala A C A G C C G T A G T G A T T A T T C T A A C T A T T G C T 250 260 270

Gly Asn Ile Leu Val Ile Met Ala Val Ser GGAAACATACTCGTCATCATGGCAGTGTCC 280 290 300

Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn CTAGAGAAAACCAACCAACCAACAAAC 320 330

Tyr Phe Leu Met Ser Leu Ala Ile Ala Asp
TATTCCTGATGTCACTTGCCATAGCTGAT
340
350

Met Leu Leu Gly Phe Leu Val Met Pro Val ATGCTGGGTTTCCTTGTCATGCCCGTG 390

Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg
T C C A T G T T A A C C A T C C T G T A T .G G G T A C C G G
400 410 420

### FIGURE 2 (cont.)

Trp Pro Leu Pro Ser Lys Leu Cys Ala Val TGGCCTCTGCCGAGCAAGCTTTTGTGCAGTC 430 440 450

Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr TGGATTTACCTGGACGTGCTCTTCTCACG 460 470 480

Leu Asp Arg Tyr Val Ala Ile Gln Asn Pro CTGGACCGCTACGCCATCCAGAATCCC 520 530 540

Ile His His Ser Arg Phe Asn Ser Arg Thr
ATCCACCACAGCCGCTTCAACTCCAGAACT
550 560 570

Lys Ala Phe Leu Lys Ile Ile Ala Val Trp
A A G G C A T T T C T G A A A A T C A T T G C T G T T T G G

580 590 600

Thr Ile Ser Val Gly Ile Ser Met Pro Ile
A C C A T A T C A G T A G G T A T A T C C A T G C C A A T A
610 620 630

Pro Val Phe Gly Leu Gln Asp Asp Ser Lys C C A G T C T T T G G G C T A C A G G A C G A T T C G A A G 650 660

### FIGURE 2 (cont.)

Val Phe Lys Glu Gly Ser Cys Leu Leu Ala GTCTTTAAGGAGGGGAGTTGCTTACTTGCC 670 680 690

Asp Asp Asn Phe Val Leu Ile Gly Ser Phe GATGATAAACTTTGTCCTGATCGGCTCTTTT
700 710 720

Val Ser Phe Phe Ile Pro Leu Thr Ile Met GTGTCATTTCCCTTAACCATCATG
730 740 750

Val Ile Thr Tyr Phe Leu Thr Ile Lys Ser GTGATCACCTACTTTCTAACTATCAAGTCA
760 770 780

Leu Gln Lys Glu Ala Thr Leu Cys Val Ser CTCCAGAAAGAAGCTACTTTGTGTGTAAGT 800 810

Asp Leu Gly Thr Arg Ala Lys Leu Ala Ser GATCTTGGCACACGGGCCAAATTAGCTTCT 830 840

Phe Ser Phe Leu Pro Gln Ser Ser Leu Ser TTCAGCTTCCTCAGAGTTCTTTGTCT
850 860 870

Ser Glu Lys Leu Phe Gln Arg Ser Ile His T C A G A A A A G C T C T T C C A G C G T C G A T C C A T 890 900

## FIGURE 2 (cont.)

Arg Glu Pro Gly Ser Tyr Thr Gly Arg Arg
A G G G A G C C A G G T C C T A C A C A G G C A G G A G G
910 920 930

Thr Met Gln Ser Ile Ser Asn Glu Gln Lys

A C T A T G C A G T C C A T C A G C A A T G A G C A A A A G

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Ala Cys Lys Val Leu Gly Ile Val Phe Phe G C A T G C A A G G T G C T G G G C A T C G T C T T C T T C 970 980 990

IleThrAsnIleMetAlaValIleCysLysATCACAAACATCATGGCCGTCATCTGCAAA103010401050

Glu Ser Cys Asn Glu Asp Val Ile Gly Ala GAGTCCTGCAATGAGGATGTCATTGGGGCCC 1060 1070 1080

Leu Leu Asn Val Phe Val Trp Ile Gly Tyr
CTGCTCAATGTTTTGGATCGGTTAT
1090 1100- 1110

Leu Ser Ser Ala Val Asn Pro Leu Val Tyr
CTCTTCAGCAGTCAACCCAACTAGTCTAC
1120 1130 1140

### FIGURE 2 (cont.)

Thr Leu Phe Asn Lys Thr Tyr Arg Ser Ala A C A C T G T T C A A C A A G A C C T A T A G G T C A G C C 1150 1170

Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys TTTTCACGGTATATTCAGTGTCAGTACAAG 1180 1190 1200

Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu G A A A A A A A A C C A T T G C A G T T A A T T T T A 1210 1230

Val Asn Thr Ile Pro Ala Leu Ala Tyr Lys
GTGAACACAATACCGGCTTTGGCCTACAAG
1240 1250 1260

Ser Ser Gln Leu Gln Met Gly Gln Lys Lys TCTAGCCAACTTCAAATGGGACAAAAAA 1270 1280 1290

Asn Ser Lys Gln Asp Ala Lys Thr Thr Asp
A A T T C A A A G C A A G A T G C C A A G A C A A C A G A T

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Asn Asp Cys Ser Met Val Ala Leu Gly Lys
A A T G A C T G C T C A A T G G T T G C T C T A G G A A A G

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Gln His Ser Glu Glu Ala Ser Lys Asp Asn CAGCATTCTAAAGACAAT

1360 1370 1380

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# FIGURE 2 (cont.)

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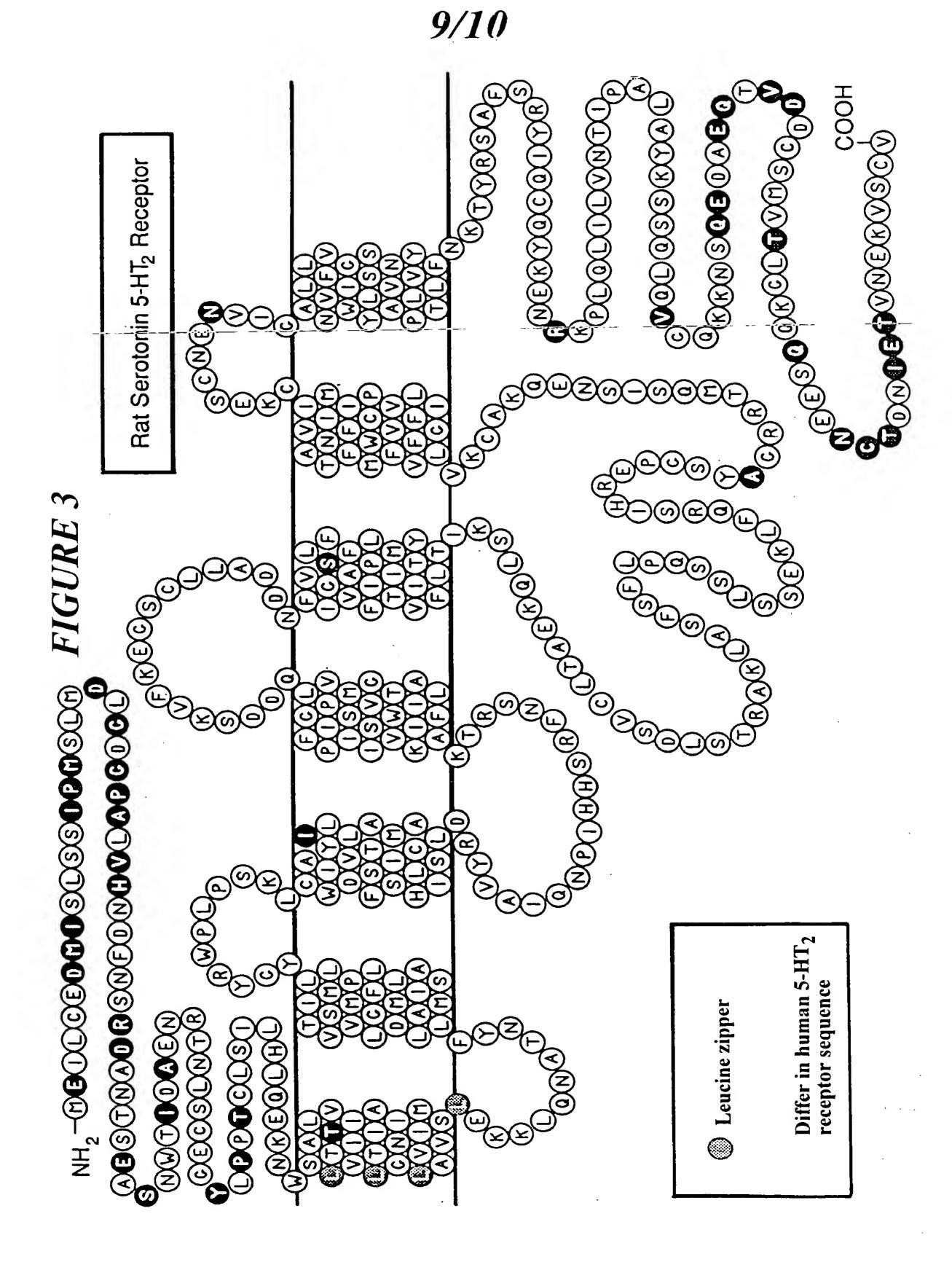
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Arg	C G T	1430
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# FIGURE 4

